<110> Shen, Ben
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<120> METHODS OF DIRECTING C-O BOND FORMATION UTILIZING A TYPE II POLYKETIDE SYNTHASE SYSTEM

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<211> 1281
<212> DNA
<213> Streptomyces griseus

<400> 2
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tgcctctccc cgtacgccca tcccgaactc cccctccgta tcgccgggac cgtgaacggc 180

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accgagcgct actacgccct ggcccgggac gaggggtcg ccgccctcgg catggagtac 420

tggctcaacg ggaccccgcc cagtgtggtg ggcaccgtgg cctccggcct ccggctgccc 480

tgccagacgc tgagcgtggc gggctcctgc aatgtggcgc tgcggacgct ccacctcgtc 540

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gtggacccgg tcttcgtggc aggcaccagc cacaccggac gcagcggcta ccgcgcgtcc 660

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<210> 3
<211> 426
<212> PRT
<213> Streptomyces griseus

<400> 3

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Leu Pro Gly Pro Asp Gly Arg Ala Cys Thr Asp Leu Asp Thr Phe Trp
20 25 30

Gly Val Val Arg Asp Gly Ala Ser Cys Leu Ser Pro Tyr Ala His Pro
35 40 45

Glu Leu Pro Leu Arg Ile Ala Gly Thr Val Asn Gly Trp Asp Pro Glu
50 55 60

Thr Glu Leu Pro Leu Ser Glu Arg Gln Ile Arg Arg Ser Ser Arg Ala
65 70 75 80

Gly Leu Met Ala Thr Gly Ala Val His Arg Ala Leu Glu His Ala Gly
85 90 95

Leu Ser Ala Asp Asp Leu Asp Pro Gly Arg Thr Ala Leu Val Ala Cys
100 105 110

Ser Leu Gln Phe Ala Phe Pro Glu Thr Glu Arg Tyr Tyr Ala Leu Ala
115 120 125

Arg Asp Glu Gly Val Ala Ala Leu Gly Met Glu Tyr Trp Leu Asn Gly
130 135 140

Thr Pro Pro Ser Val Val Gly Thr Val Ala Ser Gly Leu Arg Leu Pro
145 150 155 160

Cys Gln Thr Leu Ser Val Ala Gly Ser Cys Asn Val Ala Leu Arg Thr
165 170 175

Leu His Leu Val Gln Gln Met Phe Arg Cys Gly Asp Ile Asp Arg Ala
180 185 190

Ile Val Val Gly Val Asp Thr Thr Val Asp Pro Val Phe Val Ala Gly
195 200 205

Thr Ser His Thr Gly Arg Ser Gly Tyr Arg Ala Ser Ser Leu Ser Asp
210 215 220

Asp Pro Ala Asp Val Arg Pro His Asp Glu Ile Gln Thr Gly Asn Ala
225 230 235 240

Thr Gly Glu Gly Ala Leu Ala Val Val Leu Glu Asn Pro Ala Ala Thr
245 250 255

Gly Asp Arg Pro Gly Leu Leu His Arg Ala His Leu Arg Thr Ser Arg
260 265 270

Ser Asn Gly Pro Ser Thr Val Ala Thr Gly Pro Pro Ala Asn Val Val
275 280 285

Gly Asp Val Leu Ala Thr Leu Ala Ser Ala Arg Arg Gly Leu Gly Asp
290 295 300

Leu Ala Phe Val Asn Asp Tyr Ala Asp Gly Asn Arg Phe Val Glu Asp
305 310 315 320

His Leu Cys Gln Ala Leu Ala Gly Val Lys Glu Ala Ala Gly Tyr Gly
325 330 335

Gly Glu Leu Arg Leu Thr Asn Gln Glu Ala Val Phe Gly His Val Ala
340 345 350

Gly Thr Gly Gly Leu Val Lys Leu Leu Gly Ser Leu Leu Met Leu Arg
355 360 365

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His Gly His Ile Ala Pro Ser Ala Asn Thr Leu Val Pro Tyr Ala Gly
    370                 375                 380

Leu Pro Gly Asp Pro Val Leu Ala Gly Gly Leu Ala Thr Gly Gly Asp
385                 390                 395                 400

Ser Ala Leu Val Leu Ala Ser Gly Ala Gly Gly Asp Ala Thr Ser Met
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Val Ile Glu Tyr Glu Gly Gly Asp Leu Pro
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<210> 4
<211> 1278
<212> DNA
<213> Streptomyces griseus

<400> 4

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cgcggtgccc gcgaggcgtt cggagagctg ctgccggaca taccggcccg ctatctgcgc    180

agctacgccg acgtccacct ctacgggctg atctcgctgg ccgaggcctg ccgggacgcc    240

ggactcgatt acgggaaagg cgagttgaga ggggcggacg tgctgaccgc ccgggccggg    300

gtggacagca actacgacag ctaccgcgcc tggcacgacg ccgatccggc gacggtcact    360

ccctcggacg ccaagtccct cttcgtacgg ctcctggtgg cgggcacctc cagcgacgtc    420

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tgcgcctcct cctcggtgct gctcggcatc gcccgcatga tgatcgcctc cggccagagc    540

gacctggtcg tggtcaccgg ggtggaccgc ttcgacaccg aacgggtgct gcacggacac    600

cggttgcgcg aggtcgtcga gcgcgagggc gtgacggtgc ggcacaacag cgatccgccg    660

gcagcacccc gtcacgaccg gccgatgcgc ccgtacgacg cggcgggcga ctgcatgaac    720

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gcccggacgc acggggcggt cctcggccag gccaccacgc gcgggggcct gaacagcgcc    840

gtcgccatcg acaccggcgg tacggggctg gccgaagcgg cccgccgcgc cctgggcgac    900

catacctcgc tggggcggat cccctacgtc aacgggggcg gcgagggcga cgcgctgttc    960

acccggatcg agtccaacgc cgtccgcgcc ctgtggggcg accggtccga gcaggtgctg   1020

gtgagttcgc aggaggcgtg cttcgggcac agcggcgcgc cgctcggcaa tctgggcacg   1080

gcgctgacgc tgatgatgat gcgcgaggga gaggtctgcc ccacggccaa ctgcgcgacc   1140

ccgtcgcccg tctgcacatt cgacccggtc cccggcacca ggacgcgtgc gctgggcttc   1200
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ggtggcgatg tctgctga 1278

<210> 5
<211> 425
<212> PRT
<213> Streptomyces griseus

<400> 5

Met Gly Phe Cys Leu Pro Gly Ala Gly Asp Glu Pro Val Arg Thr Ala
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Glu Gln Val Trp Ala Ala Ala Ser Thr Gly Thr Ser His Val Glu Arg
20 25 30

Asp Gly Phe His His Gly Thr Val Arg Gly Ala Arg Glu Ala Phe Gly
35 40 45

Glu Leu Leu Pro Asp Ile Pro Ala Arg Tyr Leu Arg Ser Tyr Ala Asp
50 55 60

Val His Leu Tyr Gly Leu Ile Ser Leu Ala Glu Ala Cys Arg Asp Ala
65 70 75 80

Gly Leu Asp Tyr Gly Lys Gly Glu Leu Arg Gly Ala Asp Val Leu Thr
85 90 95

Ala Arg Ala Gly Val Asp Ser Asn Tyr Asp Ser Tyr Arg Ala Trp His
100 105 110

Asp Ala Asp Pro Ala Thr Val Thr Pro Ser Asp Ala Lys Ser Leu Phe
115 120 125

Val Arg Leu Leu Val Ala Gly Thr Ser Ser Asp Val Gly Pro Val Gln
130 135 140

Ala Ala Leu Leu Gly Ser Thr Gly Ala Asn Tyr Thr Val Ser Cys Gly
145 150 155 160

Cys Ala Ser Ser Ser Val Leu Leu Gly Ile Ala Arg Met Met Ile Ala
165 170 175

Ser Gly Gln Ser Asp Leu Val Val Val Thr Gly Val Asp Arg Phe Asp
180 185 190

Thr Glu Arg Val Leu His Gly His Arg Leu Arg Glu Val Val Glu Arg
195 200 205

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Glu Gly Val Thr Val Arg His Asn Ser Asp Pro Pro Ala Ala Pro Arg
    210                 215                 220

His Asp Arg Pro Met Arg Pro Tyr Asp Ala Ala Gly Asp Cys Met Asn
225                 230                 235                 240

Tyr Gly Asp Gly Ser Val Thr Leu Ile Leu Glu Ser Arg Glu His Ala
                245                 250                 255

Ala Ala Arg Gly Ala Arg Thr His Gly Ala Val Leu Gly Gln Ala Thr
            260                 265                 270

Thr Arg Gly Gly Leu Asn Ser Ala Val Ala Ile Asp Thr Gly Gly Thr
        275                 280                 285

Gly Leu Ala Glu Ala Ala Arg Arg Ala Leu Gly Asp His Thr Ser Leu
    290                 295                 300

Gly Arg Ile Pro Tyr Val Asn Gly Gly Gly Glu Gly Asp Ala Leu Phe
305                 310                 315                 320

Thr Arg Ile Glu Ser Asn Ala Val Arg Ala Leu Trp Gly Asp Arg Ser
                325                 330                 335

Glu Gln Val Leu Val Ser Ser Gln Glu Ala Cys Phe Gly His Ser Gly
            340                 345                 350

Ala Pro Leu Gly Asn Leu Gly Thr Ala Leu Thr Leu Met Met Met Arg
        355                 360                 365

Glu Gly Glu Val Cys Pro Thr Ala Asn Cys Ala Thr Pro Ser Pro Val
    370                 375                 380

Cys Thr Phe Asp Pro Val Pro Gly Thr Arg Thr Arg Ala Leu Gly Phe
385                 390                 395                 400

Asp Arg Ala Leu Ser Phe Asn Tyr Gln Val Gly Gly Val Asn Ser Ala
                405                 410                 415

Leu Leu Leu Gly Gly Gly Asp Val Cys
            420                 425
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<210> 6
<211> 1658
<212> DNA
<213> Streptomyces griseus

<400> 6

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cgctgggagt cgtcccgggc gaactggtgc tgagctggct gcccaacgga cccgacgcgc 240

tgcgcgcctg gtacggggtc aacctggcgg gcgcggtccc ggtgccgctc aacatcgccc 300

accggggtgc gatcctgcgt caggtgatcg ccgacagcgg ggccgaggtg ctgatctgcc 360

ggccgtcgct ggcggcccgg ctggaggatt cggacgacgc ggtgggggcg gtgcgcacgg 420

tggtcctgct gccggggccc gaggacgcgg cccaggacgt ggaggcgctc gccgggcggc 480

tggccacgcg cttccgggtg gagaccgcac tgcgcgcgga ccgggcggag ttcgcggagc 540

cggtgcccgc cccccggccg tgggacccgc agaccgtcat ctacacctcc gggacgaccg 600

gtccgtccaa gggcgtcgtc tcctcctacg cgcacctgta cagcagttgc accgccgcgt 660

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gcggcacgat cggcgcgtac gggatgctgg tgcacggcgg ttcggtgacg gtcgtgcccg 780

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ccgcgggcat ccggatacgc agggagaaga tcgtatga 1658

<210> 7
<211> 555
<212> PRT
<213> Streptomyces griseus

<400> 7

Met Ile Asp Asp Val Leu Asp Pro Ala Ser Ala Ala Val Pro Thr Ala
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Glu Gln Cys Val Leu Gly Pro Leu Leu Arg Arg Arg Ala Ala Ala Ala
20 25 30

Pro Ala Ala Pro Tyr Ala Leu Met Pro Asp Gly Asp Leu Trp Thr Tyr
35 40 45

Ala Arg Thr Leu Arg Glu Thr Glu Glu Thr Ala Ala Ala Leu Gln Ala
50 55 60

Leu Gly Val Val Pro Gly Glu Leu Val Leu Ser Trp Leu Pro Asn Gly
65 70 75 80

Pro Asp Ala Leu Arg Ala Trp Tyr Gly Val Asn Leu Ala Gly Ala Val
85 90 95

Leu Val Pro Leu Asn Ile Ala Tyr Arg Gly Ala Ile Leu Arg Gln Val
100 105 110

Ile Ala Asp Ser Gly Ala Glu Val Leu Ile Cys Arg Pro Ser Leu Ala
115 120 125

Ala Arg Leu Glu Asp Ser Asp Asp Ala Val Gly Ala Val Arg Thr Val
130 135 140

Val Leu Leu Pro Gly Pro Glu Asp Ala Ala Gln Asp Val Glu Ala Leu
145 150 155 160

Ala Gly Arg Leu Ala Thr Arg Phe Arg Val Glu Thr Ala Leu Arg Ala
165 170 175

Asp Arg Ala Glu Phe Ala Glu Pro Val Pro Ala Pro Arg Pro Trp Asp
180 185 190

Pro Gln Thr Val Ile Tyr Thr Ser Gly Thr Thr Gly Pro Ser Lys Gly
195 200 205

Val Val Ser Ser Tyr Ala His Leu Tyr Ser Ser Cys Thr Ala Ala Phe
210 215 220

His Gly Met Ala Gly Pro Glu Asp Arg Tyr Leu Leu Gln Leu Pro Leu
225 230 235 240

Phe His Ala Gly Gly Thr Ile Gly Ala Tyr Gly Met Leu Val His Gly
245 250 255

Gly Ser Val Thr Val Val Pro Ala Phe Thr Thr Gly Glu Phe Trp Pro
260 265 270

Leu Ile Arg Arg Thr Gly Thr Thr Leu Cys Thr Leu Leu Gly Val Met
275 280 285

Ala Thr Tyr Leu Leu Lys Gln Pro Pro Leu Pro Gln Asp Thr Ala His
290 295 300

Pro Leu Arg Ala Ala Tyr Val Ile Pro Phe Thr Glu Gly Ala Thr Glu
305 310 315 320

Phe Ser Lys Arg Phe Gly Val Pro Val Arg Ala Leu Phe Asn Met Thr
325 330 335

Glu Val Ser Cys Pro Val Leu Ser Ala Pro Asp His His Pro Gly Val
340 345 350

Pro Met His Cys Gly Glu Pro Arg Pro Gly Ile Ala Ala Arg Val Val
355 360 365

Asp Asp His Asp Arg Glu Val Ala Asp Gly Glu Ala Gly Glu Leu Val
370 375 380

Leu Arg Ala Asp Arg Pro Trp Ser Phe Leu Ser Gly Tyr Leu Gly Arg
385 390 395 400

Pro Ala Glu Thr Ala Ala Val Trp Arg Asn Gly Trp Phe His Thr Gly
405 410 415

Asp Thr Phe Arg Arg Ala Pro Asp Gly Gly Leu Val Phe Val Asp Arg
420 425 430

Lys Lys Asp Ala Ile Arg Arg Arg Gly Glu Asn Ile Ser Ser Phe Glu
435 440 445

Val Glu Ala Gln Ala Val Ala His Pro Gly Val Leu Glu Ala Ala Ala
450 455 460

Val Ala Val Pro Gly Asp Glu Gly Glu Asp Glu Val Leu Leu Val Val
465 470 475 480

Ala Asp Arg Asp Pro Ser Ala Pro Val Asp Pro Ala Ala Leu Leu Glu
485 490 495

Phe Leu Arg Glu Arg Leu Ala His Phe Met Leu Pro Arg Tyr Ile Arg

500 505 510

Val Leu Pro Glu Leu Pro Lys Thr Pro Thr Gly Lys Pro Thr Lys His
515 520 525

Thr Leu Arg Ala Glu Gly Val Val Ala Gly Thr Trp Asp Arg Glu Ala
530 535 540

Ala Gly Ile Arg Ile Arg Arg Glu Lys Ile Val
545 550 555